

Olivier Gascuel

List of Publications by Year in descending order

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48,982
citations

134610

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docs citations

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times ranked

60989
citing authors

#	ARTICLE	IF	CITATIONS
1	A Simple, Fast, and Accurate Algorithm to Estimate Large Phylogenies by Maximum Likelihood. <i>Systematic Biology</i> , 2003, 52, 696-704.	2.7	15,438
2	New Algorithms and Methods to Estimate Maximum-Likelihood Phylogenies: Assessing the Performance of PhyML 3.0. <i>Systematic Biology</i> , 2010, 59, 307-321.	2.7	15,166
3	SeaView Version 4: A Multiplatform Graphical User Interface for Sequence Alignment and Phylogenetic Tree Building. <i>Molecular Biology and Evolution</i> , 2010, 27, 221-224.	3.5	5,075
4	An Improved General Amino Acid Replacement Matrix. <i>Molecular Biology and Evolution</i> , 2008, 25, 1307-1320.	3.5	2,748
5	Approximate Likelihood-Ratio Test for Branches: A Fast, Accurate, and Powerful Alternative. <i>Systematic Biology</i> , 2006, 55, 539-552.	2.7	2,426
6	SMS: Smart Model Selection in PhyML. <i>Molecular Biology and Evolution</i> , 2017, 34, 2422-2424.	3.5	1,572
7	FastME 2.0: A Comprehensive, Accurate, and Fast Distance-Based Phylogeny Inference Program: Table 1.. <i>Molecular Biology and Evolution</i> , 2015, 32, 2798-2800.	3.5	1,103
8	Survey of Branch Support Methods Demonstrates Accuracy, Power, and Robustness of Fast Likelihood-based Approximation Schemes. <i>Systematic Biology</i> , 2011, 60, 685-699.	2.7	912
9	NGPhylogeny.fr: new generation phylogenetic services for non-specialists. <i>Nucleic Acids Research</i> , 2019, 47, W260-W265.	6.5	489
10	Fast and Accurate Phylogeny Reconstruction Algorithms Based on the Minimum-Evolution Principle. <i>Journal of Computational Biology</i> , 2002, 9, 687-705.	0.8	417
11	Fast Dating Using Least-Squares Criteria and Algorithms. <i>Systematic Biology</i> , 2016, 65, 82-97.	2.7	336
12	Empirical profile mixture models for phylogenetic reconstruction. <i>Bioinformatics</i> , 2008, 24, 2317-2323.	1.8	292
13	Neighbor-Joining Revealed. <i>Molecular Biology and Evolution</i> , 2006, 23, 1997-2000.	3.5	252
14	Identification of novel peptide hormones in the human proteome by hidden Markov model screening. <i>Genome Research</i> , 2007, 17, 320-327.	2.4	231
15	Phylogenetic mixture models for proteins. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2008, 363, 3965-3976.	1.8	202
16	Theoretical Foundation of the Balanced Minimum Evolution Method of Phylogenetic Inference and Its Relationship to Weighted Least-Squares Tree Fitting. <i>Molecular Biology and Evolution</i> , 2003, 21, 587-598.	3.5	201
17	Modeling Protein Evolution with Several Amino Acid Replacement Matrices Depending on Site Rates. <i>Molecular Biology and Evolution</i> , 2012, 29, 2921-2936.	3.5	201
18	Genomics, biogeography, and the diversification of placental mammals. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 14395-14400.	3.3	158

#	ARTICLE	IF	CITATIONS
19	A Fast Likelihood Method to Reconstruct and Visualize Ancestral Scenarios. <i>Molecular Biology and Evolution</i> , 2019, 36, 2069-2085.	3.5	153
20	Accounting for Solvent Accessibility and Secondary Structure in Protein Phylogenetics Is Clearly Beneficial. <i>Systematic Biology</i> , 2010, 59, 277-287.	2.7	107
21	Quartet-Based Phylogenetic Inference: Improvements and Limits. <i>Molecular Biology and Evolution</i> , 2001, 18, 1103-1116.	3.5	93
22	Reconstructing the Duplication History of Tandemly Repeated Genes. <i>Molecular Biology and Evolution</i> , 2002, 19, 278-288.	3.5	71
23	SDM: A Fast Distance-Based Approach for (Super)Tree Building in Phylogenomics. <i>Systematic Biology</i> , 2006, 55, 740-755.	2.7	69
24	Sampling bias and incorrect rooting make phylogenetic network tracing of SARS-COV-2 infections unreliable. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 12522-12523.	3.3	68
25	Branch Lengths on Birth-Death Trees and the Expected Loss of Phylogenetic Diversity. <i>Systematic Biology</i> , 2012, 61, 195-203.	2.7	67
26	On the Optimization Principle in Phylogenetic Analysis and the Minimum-Evolution Criterion. <i>Molecular Biology and Evolution</i> , 2000, 17, 401-405.	3.5	64
27	Concomitant emergence of the antisense protein gene of HIV-1 and of the pandemic. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 11537-11542.	3.3	64
28	Improvement of Distance-Based Phylogenetic Methods by a Local Maximum Likelihood Approach Using Triplets. <i>Molecular Biology and Evolution</i> , 2002, 19, 1952-1963.	3.5	63
29	Deep Conservation of Human Protein Tandem Repeats within the Eukaryotes. <i>Molecular Biology and Evolution</i> , 2014, 31, 1132-1148.	3.5	62
30	Mathematical and Computational Evolutionary Biology (2013). <i>Systematic Biology</i> , 2015, 64, 1-2.	2.7	52
31	Gotree/Goalign: toolkit and Go API to facilitate the development of phylogenetic workflows. <i>NAR Genomics and Bioinformatics</i> , 2021, 3, lqab075.	1.5	50
32	Protein export in prokaryotes and eukaryotes: Indications of a difference in the mechanism of exportation. <i>Journal of Molecular Evolution</i> , 1986, 24, 130-142.	0.8	46
33	Strengths and Limitations of the Minimum Evolution Principle. <i>Systematic Biology</i> , 2001, 50, 621-627.	2.7	45
34	TCS: a web server for multiple sequence alignment evaluation and phylogenetic reconstruction: Figure 1.. <i>Nucleic Acids Research</i> , 2015, 43, W3-W6.	6.5	44
35	A phylotype-based analysis highlights the role of drug-naïve HIV-positive individuals in the transmission of antiretroviral resistance in the UK. <i>Aids</i> , 2015, 29, 1917-1925.	1.0	41
36	Efficient Biased Estimation of Evolutionary Distances When Substitution Rates Vary Across Sites. <i>Molecular Biology and Evolution</i> , 2002, 19, 534-543.	3.5	40

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37	Inferring epidemiological parameters from phylogenies using regression-ABC: A comparative study. PLoS Computational Biology, 2017, 13, e1005416.	1.5	39
38	Predicting the Ancestral Character Changes in a Tree is Typically Easier than Predicting the Root State. Systematic Biology, 2014, 63, 421-435.	2.7	31
39	The combinatorics of overlapping genes. Journal of Theoretical Biology, 2017, 415, 90-101.	0.8	29
40	Consistency of Topological Moves Based on the Balanced Minimum Evolution Principle of Phylogenetic Inference. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2009, 6, 110-117.	1.9	27
41	Duplication and Inversion History of a Tandemly Repeated Genes Family. Journal of Computational Biology, 2007, 14, 462-478.	0.8	26
42	In-depth analysis of HIV-1 drug resistance mutations in HIV-infected individuals failing first-line regimens in West and Central Africa. Aids, 2016, 30, 2577-2589.	1.0	24
43	The Combinatorics of Tandem Duplication Trees. Systematic Biology, 2003, 52, 110-118.	2.7	23
44	Drug resistance mutations in HIV: new bioinformatics approaches and challenges. Current Opinion in Virology, 2021, 51, 56-64.	2.6	23
45	Data Model and Classification by Trees: The Minimum Variance Reduction (MVR) Method. Journal of Classification, 2000, 17, 67-99.	1.2	22
46	Performance Analysis of Hierarchical Clustering Algorithms. Journal of Classification, 2004, 21, 3-18.	1.2	21
47	A reduction algorithm for approximating a (nonmetric) dissimilarity by a tree distance. Journal of Classification, 1996, 13, 129-155.	1.2	20
48	Inferring ancestral sequences in taxon-rich phylogenies. Mathematical Biosciences, 2010, 227, 125-135.	0.9	20
49	The Origin and Evolutionary History of HIV-1 Subtype C in Senegal. PLoS ONE, 2012, 7, e33579.	1.1	20
50	Sexually-Transmitted/Founder HIV-1 Cannot Be Directly Predicted from Plasma or PBMC-Derived Viral Quasispecies in the Transmitting Partner. PLoS ONE, 2013, 8, e69144.	1.1	18
51	On the consistency of the minimum evolution principle of phylogenetic inference. Discrete Applied Mathematics, 2003, 127, 63-77.	0.5	17
52	Topological Rearrangements and Local Search Method for Tandem Duplication Trees. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2005, 2, 15-28.	1.9	16
53	Robustness of Phylogenetic Inference Based on Minimum Evolution. Bulletin of Mathematical Biology, 2010, 72, 1820-1839.	0.9	15
54	Distribution-free performance bounds with the resubstitution error estimate. Pattern Recognition Letters, 1992, 13, 757-764.	2.6	14

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55	Combinatorics of distance-based tree inference. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 16443-16448.	3.3	13
56	Generalized Bootstrap Supports for Phylogenetic Analyses of Protein Sequences Incorporating Alignment Uncertainty. Systematic Biology, 2018, 67, 997-1009.	2.7	12
57	A Darwinian Uncertainty Principle. Systematic Biology, 2020, 69, 521-529.	2.7	12
58	Twelve Numerical, Symbolic and Hybrid Supervised Classification Methods. International Journal of Pattern Recognition and Artificial Intelligence, 1998, 12, 517-571.	0.7	10
59	A "Stochastic Safety Radius"™ for Distance-Based Tree Reconstruction. Algorithmica, 2016, 74, 1386-1403.	1.0	10
60	The Role of Phylogenetics as a Tool to Predict the Spread of Resistance. Journal of Infectious Diseases, 2017, 216, S820-S823.	1.9	10
61	EuPathDomains: The divergent domain database for eukaryotic pathogens. Infection, Genetics and Evolution, 2011, 11, 698-707.	1.0	8
62	Using machine learning and big data to explore the drug resistance landscape in HIV. PLoS Computational Biology, 2021, 17, e1008873.	1.5	8
63	Improving pairwise comparison of protein sequences with domain co-occurrence. PLoS Computational Biology, 2018, 14, e1005889.	1.5	7
64	Identification of Divergent Protein Domains by Combining HMM-HMM Comparisons and Co-Occurrence Detection. PLoS ONE, 2014, 9, e95275.	1.1	6
65	Genome-wide diversity of Zika virus: Exploring spatio-temporal dynamics to guide a new nomenclature proposal. Virus Evolution, 2022, 8, veac029.	2.2	5
66	An exact and polynomial distance-based algorithm to reconstruct single copy tandem duplication trees. Journal of Discrete Algorithms, 2005, 3, 362-374.	0.7	4
67	A tutorial on the balanced minimum evolution problem. European Journal of Operational Research, 2022, 300, 1-19.	3.5	4
68	Cuban history of CRF19 recombinant subtype of HIV-1. PLoS Pathogens, 2021, 17, e1009786.	2.1	3
69	Distribution and asymptotic behavior of the phylogenetic transfer distance. Journal of Mathematical Biology, 2019, 79, 485-508.	0.8	2